

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Denney Jr., Dan W.
- (ii) TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And Leukemia
- (iii) NUMBER OF SEQUENCES: 77
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Medlen & Carroll, LLP
 - (B) STREET: 220 Montgomery Street, Suite 2200
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: United States Of America
 - (F) ZIP: 94104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/644,664
 - (B) FILING DATE: 01-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ingolia, Diane E.
 - (B) REGISTRATION NUMBER: 40,027
 - (C) REFERENCE/DOCKET NUMBER: DENNEY-02406
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 705-8410
 - (B) TELEFAX: (415) 397-8338

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTAGAGCGG CCGCGGAGGC CGAATTCTG

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCCGAATT CGGCCTCCGC GGCGCTCTA GATGCA 36

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 677 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCAGAC ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAACTA GAATGCAGTG 60
AAAAAAATGC TTTATTTGTG AAATTTGTGA TGCTATTGCT TTATTTGTAA CCATTATAAG 120
CTGCAATAAA CAAGTTAACCA ACAACAATTG CATTCACTT ATGTTTCAGG TTCAGGGGGA 180
GGTGTGGGAG GTTTTTAAA GCAAGTAAAA CCTCTACAAA TGTGGTATGG CTGATTATGA 240
TCATGAACAG ACTGTGAGGA CTGAGGGGCC TGAAATGAGC CTTGGGACTG TGAATCAATG 300
CCTGTTCAT GCCCTGAGTC TTCCATGTTC TTCTCCCCAC CATCTTCATT TTTATCAGCA 360
TTTCCTGGC TGTCTTCATC ATCATCATCA CTGTTCTTA GCCAATCTAA AACTCCAATT 420
CCCATAGCCA CATTAAACTT CATTGGTGA TACACTGACA AACTAAACTC TTTGTCCAAT 480
CTCTCTTCC ACTCCACAAT TCTGCTCTGA ATACTTGAG CAAACTCAGC CACAGGTCTG 540
TACCAAATTA ACATAAGAAG CAAAGCAATG CCACTTGAA TTATTCTCTT TTCTAACAAA 600
AACTCACTGC GTTCCAGGCA ATGCTTAAA TAATCTTGG GCCTAAAATC TATTTGTTT 660
ACAAATCTGG CCTGCAG 677

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTAGAATTCA CGCGTAGGCC TCCGCGGCCG CGCGCATGC

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AATTGCATGC GCGCGGCCGC GGAGGCCTAC GCGTGAATT

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAAGCTTGCT GTGGAATGTG TGTCAGTTAG GGTGTGGAAA GTCCCCAGGC TCCCCAGCAG	60
GCAGAAAGTAT GCAAAGCATG CATCTCAATT AGTCAGCAAC CAGGTGTGGA AAGTCCCCAG	120
GCTCCCCAGC AGGCAGAAAGT ATGCAAAGCA TGCACTCTAA TTAGTCAGCA ACCATAGTCC	180
CGCCCCCTAAC TCCGCCATC CCGCCCCCTAA CTCCGCCAG TTCCGCCAT TCTCCGCCCC	240
ATGGCTGACT AATTTTTTTT ATTTATGCAG AGGCCGAGGC CGCCTCGGCC TCTGAGCTAT	300
TCCAGAAGTA GTGAGGAGGC TTTTTTGGAG GCCTAGGCTT TTGCAAAAG CTCCTCGAGC	360
TCGCATCTCT CCTTCACGCG CCCGCCGCC TACCTGAGGC CGCCATCCAC GCCGGTTGAG	420
TCGCGTTCTG CCGCCTCCCG CCTGTGGTGC CTCCCTGAACG GCGTCCGCCG TCTAGGTAAG	480
TTTAGAGCTC AGGTCGAGAC CGGGCCTTTG TCCGGCGCTC CCTTGGAGCC TACCTAGACT	540
CAGCCGGCTC TCCACGCTTT GCCTGACCCT GCCTGCTCAA CTCTACGTCT TTGTTTCGTT	600
TTCTGTTCTG CGCCGTTACA GATCGCCTCG AGG	633

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAAGCTTGC	ATTAGTCCAA	TTTGTAAAG	ACAGGATATC	AGTGGTCCAG	GCTCTAGTTT	60
TGACTCAACA	ATATCACCA	CTGAAGCCTA	TAGAGTACGA	GCCATAGATA	AAATAAAAGA	120
TTTTATTTAG	TCTCCAGAAA	AAGGGGGAA	TGAAAGACCC	CACCTGTAGG	TTTGGCAAGC	180
TAGCTTAAGT	AACGCCATT	TGCAAGGCAT	GGAAAAATAC	ATAACTGAGA	ATAGAGAAGT	240
TCAGATCAAG	GTCAGGAACA	GATGGAACAG	CTGAATATGG	GCCAAACAGG	ATATCTGTGG	300
TAAGCAGTTC	CTGCCCGGC	TCAGGGCAA	GAACAGATGG	AACAGCTGAA	TATGGGCCAA	360
ACAGGATATC	TGTGGTAAGC	AGTTCCGTCC	CCGGCTCAGG	GCCAAGAAC	GATGGTCCCC	420
AGATGCGGTC	CAGCCCTCAG	CAGTTCTAG	AGAACCATCA	GATGTTCCA	GGGTGCCCA	480
AGGACCTGAA	ATGACCCCTGT	GCCTTATTTG	AACTAACCAA	TCAGTCGCT	TCTCGCTTCT	540
GTTCGCGCGC	TTCTGCTCCC	CGAGCTCAAT	AAAAGAGCCC	ACAACCCCTC	ACTCGGGCG	600
CCAGTCCTCC	GATTGACTGA	GTGCCCCCT	CGAGG			635

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCTTTGGA	GCTAAGCCAG	CAATGGTAGA	GGGAAGATT	TGCACGTCCC	TTCCAGGC	60
CCTCCCGTC	ACCACCCCCC	CCAACCCGCC	CCGACCGGAG	CTGAGAGTAA	TTCATACAAA	120
AGGACTCGCC	CCTGCCTTGG	GGAATCCCAG	GGACCGTCGT	TAAACTCCC	CTAACGTAGA	180
ACCCAGAGAT	CGCTGCGTTC	CCGCCCCCTC	ACCCGCCCCG	TCTCGTCATC	ACTGAGGTGG	240
AGAAGAGCAT	GCGTGAGGCT	CCGGTGCCCG	TCAGTGGGCA	GAGCGCACAT	CGCCCACAGT	300
CCCCGAGAAG	TTGGGGGGAG	GGGTGGCAA	TTGAACCGGT	GCCTAGAGAA	GGTGGCGCGG	360
GGTAAACTGG	GAAAGTGATG	TCGTGTACTG	GCTCCGCCTT	TTTCCGAGG	GTGGGGGAGA	420
ACCGTATATA	AGTGCAGTAG	TCGCCGTGAA	CGTTCTTTT	CGCAACGGGT	TTGCCGCCTC	480
GAG						483

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGCTTTGGA GCTAAGCCAG CAAT

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(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTCGAGGCAG CAAACCCGTT GCG

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(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGCTTTGGA GCTAAGCCAG CAATGGTAGA GGGAAAGATTG TGCACGTCCC TTCCAGGCAG	60
CCTCCCCGTC ACCACCCCCC CCAACCCGCC CCGACCGGAG CTGAGAGTAA TTCATACAAA	120
AGGACTCGCC CCTGCCTTGG GGAATCCCAG GGACCGTCGT TAAACTCCCA CTAACGTAGA	180
ACCCAGAGAT CGCTGCGTTC CCGCCCCCTC ACCCGCCCGC TCTCGTCATC ACTGAGGTGG	240
AGAAGAGCCA TGGTGAGGC TCCGGTGCCTC GTCAGTGGGC AGAGCGCACA TCGCCCACAG	300
TCCCCGAGAA GTTGGGGGGA GGGGTCGGCA ATTGAACCGG TGCCTAGAGA AGGTGGCGCG	360
GGGTAAACTG GGAAAGTGAT GTCGTGTACT GGCTCCGCCT TTTTCCCGAG GGTGGGGGAG	420
AACCCGTATA TAAGTGCAGT AGTCGCCGTG AACGTTCTTT TTGCAACCGG TTGATCCGCC	480
AGAACACAGG TAAGTGCCGT GTGTGGTTCC CGCGGGCCTG GCCTCTTAC GGGTTATGGC	540
CCTTGCGTGC CTTGAATTAC TTCCACGCC CTGGCTGCAG TACGTGATTC TTGATCCGA	600
GCTTCGGGTT GGAAGTGGGT GGGAGAGTTC GAGGCCTTGC GCTTAAGGAG CCCCTTCGCC	660

TCGTGCTTGA GTTGAGGCCT GGCCTGGCG CTGGGGCCCC CGCGTGCAGA TCTGGTGGCA 720
 CCTTCGCGCC TGTCTCGCTG CTTTCGATAA GTCTCTAGCC ATTTAAAATT TTTGATGACC 780
 TGCTGCGACG CTTTTTTCT GGCAAGATAG TCTTGTAAT GCGGGCCAAG ATCTGCACAC 840
 TGGTATTCG GTTTTGGGG CCGCGGGCGG CGACGGGGCC CGTGCCTCCC AGCGCACATG 900
 TTCGGCGAGG CGGGGCCTGC GAGCGCGGCC ACCGAGAACG GGACGGGGGT AGTCTCAAGC 960
 TGGCCGGCCT GCTCTGGTGC CTGGCCTCGC GCCGCCGTGT ATCGCCCCGC CCTGGCGGC 1020
 AAGGCTGGCC CGGTGGCAC CAGTTGCGTG AGCGGAAAGA TGGCCGCTTC CGGGCCCTGC 1080
 TGCAGGGAGC TCAAAATGGA GGACGCGCG CTCGGGAGAG CGGGCGGGTG AGTCACCCAC 1140
 ACAAAAGGAAA AGGGCCTTTC CGTCCTCAGC CGTCGCTTCA TGTGACTCCA CGGAGTACCG 1200
 GGCGCCGTCC AGGCACCTCG ATTAGTTCTC GAGTTTG AGTACGTCGT CTTTAGGTTG 1260
 GGGGGAGGGG TTTTATGCGA TGGAGTTCC CCACACTGAG TGGGTGGAGA CTGAAGTTAG 1320
 GCCAGCTTGG CACTTGATGT AATTCTCCTT GGAATTGAGC CTTTTGAGT TTGGATCTTG 1380
 GTTCATTCTC AAGCCTCAGA CAGTGGTTCA AAGTTTTTT CTTCCATTTC AGGTGTCGTG 1440
 AAAACTCTAG A 1451

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCTAGAGTTT TCACGACACC TGA 23

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 88..741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTACCTCACT GCTTCCGGA GCGGTAGCAC CTCCTCCGCC GGCTCCTCC TCAGACCGCT 60

TTTIGCCGCG AGCCGACCGG TCCCCGTC ATG CCG ACC CGC AGT CCC AGC GTC Met Pro Thr Arg Ser Pro Ser Val	1 5	111
GTG ATT AGC GAT GAT GAA CCA GGT TAT GAC CTA GAT TTG TTT TGT ATA Val Ile Ser Asp Asp Glu Pro Gly Tyr Asp Leu Asp Leu Phe Cys Ile	10 15 20	159
CCT AAT CAT TAT GCC GAG GAT TTG GAA AAA GTG TTT ATT CCT CAT GGA Pro Asn His Tyr Ala Glu Asp Leu Glu Lys Val Phe Ile Pro His Gly	25 30 35 40	207
CTG ATT ATG GAC AGG ACT GAA AGA CTT GCT CGA GAT GTC ATG AAG GAG Leu Ile Met Asp Arg Thr Glu Arg Leu Ala Arg Asp Val Met Lys Glu	45 50 55	255
ATG GGA GGC CAT CAC ATT GTG GCC CTC TGT GTG CTC AAG GGG GGC TAT Met Gly Gly His His Ile Val Ala Leu Cys Val Leu Lys Gly Gly Tyr	60 65 70	303
AAG TTC TTT GCT GAC CTG CTG GAT TAC ATT AAA GCA CTG AAT AGA AAT Lys Phe Phe Ala Asp Leu Leu Asp Tyr Ile Lys Ala Leu Asn Arg Asn	75 80 85	351
AGT GAT AGA TCC ATT CCT ATG ACT GTA GAT TTT ATC AGA CTG AAG AGC Ser Asp Arg Ser Ile Pro Met Thr Val Asp Phe Ile Arg Leu Lys Ser	90 95 100	399
TAC TGT AAT GAT CAG TCA ACG GGG GAC ATA AAA GTT ATT GGT GGA GAT Tyr Cys Asn Asp Gln Ser Thr Gly Asp Ile Lys Val Ile Gly Gly Asp	105 110 115 120	447
GAT CTC TCA ACT TTA ACT GGA AAG AAT GTC TTG ATT GTT GAA GAT ATA Asp Leu Ser Thr Leu Thr Gly Lys Asn Val Leu Ile Val Glu Asp Ile	125 130 135	495
ATT GAC ACT GGT AAA ACA ATG CAA ACT TTG CTT TCC CTG GTT AAG CAG Ile Asp Thr Gly Lys Thr Met Gln Thr Leu Leu Ser Leu Val Lys Gln	140 145 150	543
TAC AGC CCC AAA ATG GTT AAG GTT GCA AGC TTG CTG GTG AAA AGG ACC Tyr Ser Pro Lys Met Val Lys Val Ala Ser Leu Leu Val Lys Arg Thr	155 160 165	591
TCT CGA AGT GTT GGA TAC AGG CCA GAC TTT GTT GGA TTT GAA ATT CCA Ser Arg Ser Val Gly Tyr Arg Pro Asp Phe Val Gly Phe Glu Ile Pro	170 175 180	639
GAC AAG TTT GTT GTT GGA TAT GCC CTT GAC TAT AAT GAG TAC TTC AGG Asp Lys Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg	185 190 195 200	687
AAT TTG AAT CAC GTT TGT GTC ATT AGT GAA ACT GGA AAA GCC AAA TAC Asn Leu Asn His Val Cys Val Ile Ser Glu Thr Gly Lys Ala Lys Tyr	205 210 215	735
AAA GCC TAAGATGAGC GCAAGTTGAA TCTGCAAATA CGAGGAGTCC TGTTGATGTT Lys Ala		791
GCCAGTAAAA TTAGCAGGTG TTCTAGTCCT GTGGCCATCT GCCTAGTAAA GCTTTTGCA		851

TGAACCTTCT ATGAATGTTA CTGTTTATT TTTAGAAATG TCAGTTGCTG CGTCCCCAGA	911
CTTTTGATTT GCACTATGAG CCTATAGGCC AGCCTACCCT CTGGTAGATT GTCGCTTATC	971
TTGTAAGAAA AACAAATCTC TTAAATTACC ACTTTTAAAT AATAACTTG AGATTGTATC	1031
TGTAAGAAGG ATTTAAAGAG AAGCTATATT AGTTTTTAA TTGGTATTAA AATTTTTATA	1091
TATTCAGGAG AGAAAAGATGT GATTGATATT GTTAATTAG ACGAGTCTGA AGCTCTCGAT	1151
TTCCTATCAG TAACAGCATC TAAGAGGTT TGCTCAGTGG AATAAACATG TTTCAGCAGT	1211
GTTGGCTGTA TTTCCCACT TTCAGTAAAT CGTTGTCAAC AGTTCTTT AAATGCAAAT	1271
AAATAAATTC TAAAAATT	1289

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Pro Thr Arg Ser Pro Ser Val Val Ile Ser Asp Asp Glu Pro Gly			
1	5	10	15
Tyr Asp Leu Asp Leu Phe Cys Ile Pro Asn His Tyr Ala Glu Asp Leu			
20	25	30	
Glu Lys Val Phe Ile Pro His Gly Leu Ile Met Asp Arg Thr Glu Arg			
35	40	45	
Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala			
50	55	60	
Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp			
65	70	75	80
Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr			
85	90	95	
Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly			
100	105	110	
Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys			
115	120	125	
Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln			
130	135	140	
Thr Leu Leu Ser Leu Val Lys Gln Tyr Ser Pro Lys Met Val Lys Val			
145	150	155	160
Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro			
165	170	175	
Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala			
180	185	190	

Leu Asp Tyr Asn Glu Tyr Phe Arg Asn Leu Asn His Val Cys Val Ile
195 200 205

Ser Glu Thr Gly Lys Ala Lys Tyr Lys Ala
210 215

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCATGCGCGC GGCCGCGGAG GCTTTTTTTT TTTTTTTTTT 40

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGCAACGCG TGCCATCATG GTTCGAC 27

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGCAGCGGC CGCATAGATC TAAAGCCAGC 30

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 671 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 13..573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACGCGTGCCA TC ATG GTT CGA CCA TTG AAC TGC ATC GTC GCC GTG TCC Met Val Arg Pro Leu Asn Cys Ile Val Ala Val Ser	48
1 5 10	
CAA AAT ATG GGG ATT GGC AAG AAC GGA GAC CTA CCC TGG CCT CCG CTC Gln Asn Met Gly Ile Gly Lys Asn Gly Asp Leu Pro Trp Pro Pro Leu	96
15 20 25	
AGG AAC GAG TTC AAG TAC TTC CAA AGA ATG ACC ACA ACC TCT TCA GTG Arg Asn Glu Phe Lys Tyr Phe Gln Arg Met Thr Thr Ser Ser Val	144
30 35 40	
GAA GGT AAA CAG AAT CTG GTG ATT ATG GGT AGG AAA ACC TGG TTC TCC Glu Gly Lys Gln Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser	192
45 50 55 60	
ATT CCT GAG AAG AAT CGA CCT TTA AAG GAC AGA ATT AAT ATA GTT CTC Ile Pro Glu Lys Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu	240
65 70 75	
AGT AGA GAA CTC AAA GAA CCA CCA CGA GGA GCT CAT TTT CTT GCC AAA Ser Arg Glu Leu Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys	288
80 85 90	
AGT TTG GAT GAT GCC TTA AGA CTT ATT GAA CAA CCG GAA TTG GCA AGT Ser Leu Asp Asp Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser	336
95 100 105	
AAA GTA GAC ATG GTT TGG ATA GTC GGA GGC AGT TCT GTT TAC CAG GAA Lys Val Asp Met Val Trp Ile Val Gly Ser Ser Val Tyr Gln Glu	384
110 115 120	
GCC ATG AAT CAA CCA GGC CAC CTT AGA CTC TTT GTG ACA AGG ATC ATG Ala Met Asn Gln Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met	432
125 130 135 140	
CAG GAA TTT GAA AGT GAC ACG TTT TTC CCA GAA ATT GAT TTG GGG AAA Gln Glu Phe Glu Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys	480
145 150 155	
TAT AAA CTT CTC CCA GAA TAC CCA GGC GTC CTC TCT GAG GTC CAG GAG Tyr Lys Leu Leu Pro Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu	528
160 165 170	
GAA AAA GGC ATC AAG TAT AAG TTT GAA GTC TAC GAG AAG AAA GAC Glu Lys Gly Ile Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp	573
175 180 185	
TAACAGGAAG ATGCTTCAA GTTCTCTGCT CCCCTCCTAA AGCTATGCAT TTTTATAAGA	633
CCATGGGACT TTTGCTGGCT TTAGATCTAT GCGGCCGC	671

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Val Arg Pro Leu Asn Cys Ile Val Ala Val Ser Gln Asn Met Gly
1 5 10 15

Ile Gly Lys Asn Gly Asp Leu Pro Trp Pro Pro Leu Arg Asn Glu Phe
20 25 30

Lys Tyr Phe Gln Arg Met Thr Thr Ser Ser Val Glu Gly Lys Gln
35 40 45

Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile Pro Glu Lys
50 55 60

Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser Arg Glu Leu
65 70 75 80

Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser Leu Asp Asp
85 90 95

Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys Val Asp Met
100 105 110

Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala Met Asn Gln
115 120 125

Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln Glu Phe Glu
130 135 140

Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr Lys Leu Leu
145 150 155 160

Pro Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu Glu Lys Gly Ile
165 170 175

Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp
180 185

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATATATCTAG ACCACCATGC CTGGCTCAGC ACTG

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(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATTATTGCGG CCGCTTAGCT TTTCATTTG ATCAT

35

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTCTAGAGC CAAATAAAGG AAGTGAACC ACTTCAGGTA CTACCCGTCT TCTATCTGGG 60

CACACGTGTT TCACGTTGAC AGGTTGCTT GGGACGCTAG TAACCATGGG CTTGCTGACT 120

TAGGCATCGA ATTCA 134

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTGATG CCTAAGTCAG CAAGCCATG GTTACTAGCG TCCCAAGCAA ACCTGTCAAC 60

GTGAAACACG TGTGCCAGA TAGAACACGG GTAGTACCTG AAGTGGTCC ACTTCCTTA 120

TTGGCTCTA GACC 134

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TAATACGACT CACTATAGGG CGAATTGGAG CTCCACCGCG GTGGCGGCCG CTCTAGAACT 60

AGTGGATCCC CCGGGCTGCA GGAATTGAT GGTCTAGAGC CAAATAAAGG AAGTGAACC 120

ACTTCAGGTA CTACCCGTCT TCTATCTGGG CACACGTGTT TCACGTTGAC AGGTTGCTT 180

GGGACGCTAG TAACCATGGG CTTGCTGACT TAGGCATCGA ATTCACTCAAG CTTATCGATA 240

CCGTCGACCT CGAGGGGGGG CCCGGTACCC AGCTTTGTT CCCTTTAGTG AGGGTTAATT 300

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCACTTCCTT TATTGGGAG AGGGCTTG 28

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG GCC ATA AGT GGA GTC CCT GTG CTA GGA TTT TTC ATC ATA GCT GTG Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val 1 5 10 15	48
CTG ATG AGC GCT CAG GAA TCA TGG GCT ATC AAA GAA GAA CAT GTG ATC Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile 20 25 30	96
ATC CAG GCC GAG TTC TAT CTG AAT CCT GAC CAA TCA GGC GAG TTT ATG Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met 35 40 45	144
TTT GAC TTT GAT GGT GAT GAG ATT TTC CAT GTG GAT ATG GCA AAG AAG Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys 50 55 60	192
GAG ACG GTC TGG CGG CTT GAA GAA TTT GGA CGA TTT GCC AGC TTT GAG Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu 65 70 75 80	240
GCT CAA GGT GCA TTG GCC AAC ATA GCT GTG GAC AAA GCC AAC TTG GAA Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu 85 90 95	288
ATC ATG ACA AAG CGC TCC AAC TAT ACT CCG ATC ACC AAT GTA CCT CCA Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro 100 105 110	336
GAG GTA ACT GTG CTC ACG AAC AGC CCT GTG GAA CTG AGA GAG CCC AAC Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn 115 120 125	384

GTC CTC ATC TGT TTC ATA GAC AAG TTC ACC CCA CCA GTG GTC AAT GTC Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val 130 135 140	432
ACG TGG CTT CGA AAT GGA AAA CCT GTC ACC ACA GGA GTG TCA GAG ACA Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr 145 150 155 160	480
GTC TTC CTG CCC AGG GAA GAC CAC CTT TTC CGC AAG TTC CAC TAT CTC Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu 165 170 175	528
CCC TTC CTG CCC TCA ACT GAG GAC GTT TAC GAC TGC AGG GTG GAG CAC Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His 180 185 190	576
TGG GGC TTG GAT GAG CCT CTT CTC AAG CAC TGG GAG TTT GAT GCT CCA Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro 195 200 205	624
AGC CCT CTC CCA AAT AAA GGA AGT GGA ACC ACT TCA GGT ACT ACC CGT Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg 210 215 220	672
CTT CTA TCT GGG CAC ACG TGT TTC ACG TTG ACA GGT TTG CTT GGG ACG Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr 225 230 235 240	720
CTA GTA ACC ATG GGC TTG CTG ACT TAG Leu Val Thr Met Gly Leu Leu Thr 245	747

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val 1 5 10 15
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile 20 25 30
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met 35 40 45
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys 50 55 60
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu 65 70 75 80
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu 85 90 95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110
 Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125
 Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
 130 135 140
 Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
 145 150 155 160
 Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
 165 170 175
 Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
 180 185 190
 Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
 195 200 205
 Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg
 210 215 220
 Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr
 225 230 235 240
 Leu Val Thr Met Gly Leu Leu Thr
 245

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCACTTCCTT TATTTGGTGC AGATTCA

28

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 786 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATG GTG TGT CTG AAG CTC CCT GGA GGC TCC TGC ATG ACA GCG CTG ACA Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr	48
1 5 10 15	
GTG ACA CTG ATG GTG CTG AGC TCC CGA CTG GCT TTG GCT GGG GAC ACC Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr	96
20 25 30	
CGA CCA CGT TTC TTG TGG CAG CTT AAG TTT GAA TGT CAT TTC TTC AAT Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn	144
35 40 45	
GGG ACG GAG CGG GTG CGG TTG CTG GAA AGA TGC ATC TAT AAC CAA GAG Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu	192
50 55 60	
GAG TCC GTG CGC TTC GAC AGC GAC GTG GGG GAG TAC CCG GCG GTT GAG Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu	240
65 70 75 80	
GAG CTG GGG CGG CCT GAT GCC GAG TAC TGG AAC AGC CAG AAG GAC CTC Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu	288
85 90 95	
CTG GAG CAG AAG CGG GGC CAG GTG GAC AAT TAC TGC AGA CAC AAC TAC Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr	336
100 105 110	
GGG GTT GGT GAG AGC TTC ACA GTG CAG CGG CGA GTT GAG CCT AAG GTG Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val	384
115 120 125	
ACT GTG TAT CCT TCA AAG ACC CAG CCC CTG CAG CAC CAC AAC CTC CTG Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu	432
130 135 140	
GTC TGC TCT GTG AGT GGT TTC TAT CCA GGC AGC ATT GAA GTC AGG TGG Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp	480
145 150 155 160	
TTC CGG AAC GGC CAG GAA GAG AAG GCT GGG GTG GTG TCC ACG GGC CTG Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu	528
165 170 175	
ATC CAG AAT GGA GAT TGG ACC TTC CAG ACC CTG GTG ATG CTG GAA ATA Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile	576
180 185 190	
GTT CCT CGG AGT GGA GAG GTT TAC ACC TGC CAA GTG GAG CAC CCA AGT Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser	624
195 200 205	
GTG ACG AGC CCT CTC ACA GTG GAA TGG AGA GCA CGG TCT GAA TCT GCA Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala	672
210 215 220	
CCA AAT AAA GGA AGT GGA ACC ACT TCA GGT ACT ACC CGT CTT CTA TCT Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser	720
225 230 235 240	

GGG CAC ACG TGT TTC ACG TTG ACA GGT TTG CTT GGG ACG CTA GTA ACC 768
Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
245 250 255

ATG GGC TTG CTG ACT TAG 786
Met Gly Leu Leu Thr
260

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr
1 5 10 15

Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr
20 25 30

Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn
35 40 45

Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu
50 55 60

Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu
65 70 75 80

Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
85 90 95

Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr
100 105 110

Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val
115 120 125

Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
130 135 140

Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
145 150 155 160

Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu
165 170 175

Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile
180 185 190

Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
195 200 205

Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
210 215 220

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
225 230 235 240

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
245 250 255

Met Gly Leu Leu Thr
260

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTG GAT CCA CGA TCG TTT CTA TTG CGC AAT CCA AAT GAT AAG TAC GAA 48
Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1 5 10 15

CCA TTT TGG GAA GAT ACT ACA GAG AAC GTG GTG TGT GCC CTG GGC CTG 96
Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu
20 25 30

ACT GTG GGT CTG GTG GGC ATC ATT ATT GGG ACC ATC TTC ATC ATC AAG 144
Thr Val Gly Leu Val Gly Ile Ile Gly Thr Ile Phe Ile Ile Lys
35 40 45

GGA GTG CGC AAA AGC AAT GCA GCA GAA CGC AGG GGG CCT CTG 186
Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu
50 55 60

TAA 189

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1 5 10 15

Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu
20 25 30

Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys
35 40 45

Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTG GAT CCA CGA TCG TTT CTA TTG CGC AAT CCA AAT GAT AAG TAC GAA 48
Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1 5 10 15

CCA TTT TGG GAA GAT CAG AGC AAG ATG CTG AGT GGA GTC GGG GGC TTC 96
Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe
20 25 30

GTC CTG GGC CTG CTC TTC CTT GGG GCC GGG CTG TTC ATC TAC TTC AGG 144
Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg
35 40 45

AAT CAG AAA GGA CAC TCT GGA CTT CAG CCA ACA GGA TTC CTG AGC 189
Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser
50 55 60

TGA 192

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1 5 10 15

Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe
20 25 30

Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg
35 40 45

Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGATCGTGG A TCCAAGTTA GGTTCGTATC TGTTTCAAA

39

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGATCGAGGA TCCAAGATGG TGGCAGACAG GACC

34

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ACGCGTCCAC CATGGCCATA AGTGGAGTCC CT

32

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGATCCA ACT CTGTAGTCTC TGGGAGAG

28

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ACGCGTCCAC CATGGTGTGT CTGAAGCTCC TG

32

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGATCCAAC TGCCTGTGC AGATTCAA

29

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAATTCTTT TTGCGTGTGG CAGTTTAAG TTATTAGTTT TTAAAATCAG TACTTTTAA

60

TGGAAACAAAC TTGACCAAAA ATTTGTCACA GAATTTGAG ACCCATTAAG AAAGTTAAAT

120

GAGAAACCTG TGTGTTCTT TGGTCAACAC CGAGACATTG AGGTGAAAGA CATCTAATTG

180

TGGTTTACG AATCTGGAAA CTTCTTGAAA ATGTAATTCT TGAGTTAACG CTTCTGGGTG

240

GAGAATAGGG TTGTTTCCC CCCACATAAT TGGAAGGGGA AGGAATATCG AT

292

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCGATGGCGC GCCTTAATTA

20

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGCTTAATTA AGGCGCGCCA

20

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 7..1137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCGGCC GCG TCG ACC AAG GGC CCC AGC GTG TTC CCC CTG GCC CCC TGC
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
1 5 10

48

TCC CGC AGC ACC AGC GGC GGC ACC GCC GCC CTG GGC TGC CTG GTG AAG
Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
15 20 25 30

96

GAC TAC TTC CCC GAG CCC GTG ACC GTG AGC TGG AAC AGC AGC GGC GCC CTG
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
35 40 45

144

ACC AGC GGC GTC CAC ACC TTC CCC GCC GTG CTG CAG TCC AGC GGC CTG
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
50 55 60

192

TAC TCC CTG AGC AGC GTG GTG ACC GTG CCC AGC AGC AGC CTG GGC ACC
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
65 70 75

240

CAG ACC TAC ACC TGC AAC GTG AAC CAC AAG CCC AGC AAC ACC AAG GTG
Gln Thr Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
80 85 90

288

GAC AAG CGC GTG GAG CTG AAG ACC CCC CTG GGC GAC ACC ACC CAC ACC
Asp Lys Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr
95 100 105 110

336

TGC CCC CGC TGC CCC GAG CCC AAG AGC TGC GAC ACC CCT CCC CCC TGC Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys 115 120 125	384
CCC CGC TGC CCC GAG CCC AAG AGC TGC GAC ACC CCT CCC CCC TGC CCC Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro 130 135 140	432
CGC TGC CCC GAG CCC AAG AGC TGC GAC ACC CCT CCC CCC TGC CCC CGC Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg 145 150 155	480
TGC CCC GCC CCC GAG CTG CTG GGC GGC CCC AGC GTG TTC CTG TTC CCC Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro 160 165 170	528
CCC AAG CCC AAG GAC ACC CTG ATG ATC TCC CGC ACC CCC GAG GTG ACC Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr 175 180 185 190	576
TGC GTG GTG GTG GAC GTG AGC CAC GAG GAC CCC GAG GTG CAG TTC AAG Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys 195 200 205	624
TGG TAC GTG GAC GGC GTG GAG GTG CAT AAC GCC AAG ACC AAG CCC CGC Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg 210 215 220	672
GAG GAG CAG TAC AAC AGC ACC TTC CGC GTG GTG AGC GTG CTG ACC GTG Glu Glu Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val 225 230 235	720
CTG CAC CAG GAC TGG CTG AAC GGC AAG GAG TAC AAG TGC AAG GTG AGC Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser 240 245 250	768
AAC AAG GCC CTG CCC GCC CCC ATC GAG AAG ACC ATC TCC AAG ACC AAG Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys 255 260 265 270	816
GGC CAG CCC CGC GAG CCC CAG GTG TAC ACC CTG CCC CCC AGC CGC GAG Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu 275 280 285	864
GAG ATG ACC AAG AAC CAG GTG AGC CTG ACC TGC CTG GTG AAG GGC TTC Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe 290 295 300	912
TAC CCC AGC ATC GCC GTG GAG TGG GAG AGC AGC GGC CAG CCC GAG Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu 305 310 315	960
AAC AAC TAC AAC ACC ACC CCC CCC ATG CTG GAC AGC GAC GGC AGC TTC Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe 320 325 330	1008
TTC CTG TAC AGC AAG CTG ACC GTG GAC AAG AGC AGC CGC TGG CAG CAG GGC Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly 335 340 345 350	1056

AAC ATC TTC TCC TGC AGC GTG ATG CAT GAG GCC CTG CAC AAC CGC TTC 1104
 Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
 355 360 365

ACC CAG AAG AGC CTG AGC CTG AGC CCC GGC AAG TGATAGATCT
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 377 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
130 135 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145 150 155 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
210 215 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
 225 230 235 240
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 245 250 255
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
 260 265 270
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 275 280 285
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 290 295 300
 Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
 305 310 315 320
 Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
 325 330 335
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
 340 345 350
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
 355 360 365
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 999 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 9..989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCGGCCGC	GCG	TCG	ACC	AAG	GGC	CCC	AGC	GTG	TTC	CCC	CTG	GCC	CCC	TGC		50
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys			
1																
AGC	CGC	AGC	ACC	AGC	GAG	AGC	ACC	GCC	GCC	CTG	GGC	TGC	CTG	GTG	AAG	98
Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
15																
GAC	TAC	TTC	CCC	GAG	CCC	GTG	ACC	GTG	AGC	TGG	AAC	AGC	GGC	GCC	CTG	146
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
35																
ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCC	GCC	GTG	CTG	CAG	AGC	AGC	GGC	CTG	194
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
50																

TAC TCC CTG AGC GTG GTG ACC GTG CCC AGC AGC AGC CTG GGC ACC Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr 65 70 75	242
AAG ACC TAC ACC TGC AAC GTG GAC CAC AAG CCC AGC AAC ACC AAG GTG Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val 80 85 90	290
GAC AAG CGC GTG GAG AGC AAG TAC GGC CCC CCC TGC CCC AGC TGC CCC Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro 95 100 105 110	338
GCC CCC GAG TTC CTG GGC CCC AGC GTG TTC CTG TTC CCC CCC AAG Ala Pro Glu Phe Leu Gly Pro Ser Val Phe Leu Phe Pro Pro Lys 115 120 125	386
CCC AAG GAC ACC CTG ATG ATC AGC CGC ACC CCC GAG GTG ACC TGC GTG Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val 130 135 140	434
GTG GTG GAC GTG AGC CAG GAG GAC CCC GAG GTG CAG TTC AAC TGG TAC Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr 145 150 155	482
GTG GAC GGC GTG GAG GTG CAT AAC GCC AAG ACC AAG CCC CGC GAG GAG Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu 160 165 170	530
CAG TTC AAC AGC ACC TAC CGC GTG GTG AGC GTG CTG ACC GTG CTG CAC Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His 175 180 185 190	578
CAG GAC TGG CTG AAC GGC AAG GAG TAC AAG TGC AAG GTG TCC AAC AAG Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys 195 200 205	626
GGC CTG CCC AGC AGC ATC GAG AAG ACC ATC AGC AAG GCC AAG GGC CAG Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln 210 215 220	674
CCC CGC GAG CCC CAG GTG TAC ACC CTG CCC CCC AGC CAG GAG GAG ATG Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met 225 230 235	722
ACC AAG AAC CAG GTG AGC CTG ACC TGC CTG GTG AAG GGC TTC TAC CCC Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro 240 245 250	770
AGC GAC ATC GCC GTG GAG TGG GAG AGC AAC GGC CAG CCC GAG AAC AAC Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn 255 260 265 270	818
TAC AAG ACC ACC CCC CCC GTG CTG GAC AGC GAC GGC AGC TTC TTC CTG Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu 275 280 285	866
TAC AGC CGC CTG ACC GTG GAC AAG AGC CGC TGG CAG GAG GGC AAC GTG Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val 290 295 300	914

TTC TCC TGC TCC GTG ATG CAT GAG GCC CTG CAC AAC CAC TAC ACC CAG 962
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
305 310 315

AAG AGC CTG AGC CTG AGC CTG GGC AAG TGATAGATCT 999
Lys Ser Leu Ser Leu Ser Leu Gly Lys
320 325

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320
 Leu Ser Leu Ser Leu Gly Lys
 325

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 9..326

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GC GG CG CG ACT GT G G C T G C A C C T C T G C T G C T C C G C C A T C T G C T C T G A T	50
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
1 5 10	
GAG CAG CTT AAG TCC GGA ACC GCC AGC GTG GTG TGC CTG CTG AAC AAC	98
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn	
15 20 25 30	
TTC TAC CCC CGC GAG GCC AAG GTG CAG TGG AAG GTG GAC AAC GCC CTC	146
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu	
35 40 45	
CAG AGC GGC AAC TCC CAG GAG AGC GTG ACC GAG CAG GAC AGC AAG GAC	194
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp	
50 55 60	
AGC ACC TAC AGC CTG AGC ACC CTG ACC CTG AGC AAG GCC GAC TAC	242
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr	
65 70 75	
GAG AAG CAC AAG GTG TAC GCC TGC GAG GTG ACC CAT CAG GGC CTG AGC	290
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser	
80 85 90	

AGC CCC GTG ACC AAG AGC TTC AAC CGG GGC GAG TGC TAGTGAGATC
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 95 100 105

T 337

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 9..335

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCGGCCGC ACC GTC CTA GGT CAG CCC AAG GCG GCG CCC AGC GTG ACC CTG 50
 Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu
 1 5 10

TTC CCC CCC AGC AGC GAG GAG CTG CAG GCC AAC AAG GCC ACC CTG GTG
 Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val
 15 20 25 30

TGC CTG ATC AGC GAC TTC TAC CCC GGG GCC GTG ACC GTG GCC TGG AAG Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys 35 40 45	146
GCC GAC AGC AGC CCC GTG AAG GCC GGC GTG GAG ACC ACC ACC CCC AGC Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Pro Ser 50 55 60	194
AAG CAG AGC AAC AAC AAG TAC GCC GCC AGC AGC TAC CTG AGC CTG ACC Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr 65 70 75	242
CCC GAG CAG TGG AAG AGC CAC CGC AGC TAC AGC TGC CAG GTC ACC CAC Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His 80 85 90	290
GAG GGC AGC ACC GTG GAG AAG ACC GTG GCC CCC ACC GAG TGC AGC Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser 95 100 105	335
TAGTGAGATC T	346

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro 1 5 10 15
Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu 20 25 30
Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp 35 40 45
Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Pro Ser Lys Gln 50 55 60
Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu 65 70 75 80
Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly 85 90 95
Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser 100 105

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TCTAGAATTACACGCGTCCACCATGGACTGGACCTGGAG

38

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCTAGAATTACACGCGTCCACCATGGACACACATTTGCTACAC

41

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TCTAGAATTACACGCGTCCACCATGGAGTTTGGGCTGAGCTGG

42

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TCTAGAATTACACGCGTCCACCATGAAACACCTGTGGTTCTTCCT

44

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TCTAGAATTCA CGCGTCCAC CATGGGGTCA ACCGCCATCC T

41

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TCTAGAATTCA CGCGTCCAC CATGTCTGTC TCCTTCCTCA TCTT

44

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCCTGAGTTC CACGACACCG TCAC

24

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGGGAAAAGG GTTGGGGCGG ATGC

24

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAGGGGCCCT TGGTCGACGC TGAGGAGACG GTGACCAGG

39

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAGGGGCCCT TGGTCGACGC TGAAGAGACG GTGACCATTG

40

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAGGGGCCCT TGGTCGACGC TGAGGAGACG GTGACCGTG

39

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TCTAGAATTC ACGCGTCCAC CATGGACATG AGGGTCCCCG CTCAG

45

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TCTAGAATTACCGCGTCCACCATGAGGCTCCTGCTCAGC 40

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTAGAATTACCGCGTCCACCATGGAAGGCCCCAGCGCAGC TT 42

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TCTAGAATTACCGCGTCCACCATGGTGTTGCAGACCCAGG T 41

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TCTAGAATTACCGCGTCCACCATGGGGTCC CAGGTTCACCT 41

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TCTAGAACATTACACCGCGTCCACCATGTTGCCATCACAACTCA TTG

43

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TCTAGAACATTACACCGCGTCCACCATGGTGTCC CCGTTGCAAT T

41

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGTTCCGGAC TTAAGCTGCT CATCAGATGG CGGG

34

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TCTAGAACATTACACCGCGTCCACCATGGCCTGC TCTCCTCTCC TCCT

44

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCTAGAATTC ACGCGTCCAC CATGGCCTGG GCTCTGCTGC TCCT

44

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TCTAGAATTC ACGCGTCCAC CATGGCCTGG ATCCTTCTCC TCCTC

45

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TCTAGAATTC ACGCGTCCAC CATGGCCTGG ACCCCTCTCT GGCTC

45

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TCTAGAATTC ACGCGTCCAC CATGGCCTGG GCCCCACTAC T

41

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TCTAGAATT CACCGTCCAC CATGGCCTGG ATGATGCTTC TCCT

44

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCGCCGCCT TGGGCTGACC TAGGACGGT

29